IFWO

RAW SEQUENCE LISTING   DATE: 08/27/2004
PATENT APPLICATION: **US/10/700,313**   TIME: 14:23:00

Input Set : **N:\Crf3\RULE60\10700313.raw**
Output Set: **N:\CRF4\08272004\J700313.raw**

SEQUENCE LISTING
```
 3 (1) GENERAL INFORMATION:
 5      (i) APPLICANT: Combadiere et al.,
 7     (ii) TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
 9    (iii) NUMBER OF SEQUENCES: 9
11     (iv) CORRESPONDENCE ADDRESS:
12          (A) ADDRESSEE: Fish & Richardson P.C.
13          (B) STREET: 4225 Executive Square, Suite 1400
14          (C) CITY: La Jolla
15          (D) STATE: CA
16          (E) COUNTRY: USA
17          (F) ZIP: 92037
19      (v) COMPUTER READABLE FORM:
20          (A) MEDIUM TYPE: Floppy disk
21          (B) COMPUTER: IBM PC compatible
22          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
23          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
25     (vi) CURRENT APPLICATION DATA:
```
ENTERED

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C--> 26          (A) APPLICATION NUMBER: US/10/700,313
C--> 27          (B) FILING DATE: 31-Oct-2003
W--> 37          (C) CLASSIFICATION: 536
C--> 34    (vii) PRIOR APPLICATION DATA:
31          (A) APPLICATION NUMBER: US/08/864,458
32          (B) FILING DATE: 28-MAY-1997
35          (A) APPLICATION NUMBER: Provisional 60/018,508
36          (B) FILING DATE: May 28, 1996
C--> 39   (viii) ATTORNEY/AGENT INFORMATION:
40          (A) NAME: Haile, Lisa A.
41          (B) REGISTRATION NUMBER: 38,347
42          (C) REFERENCE/DOCKET NUMBER: 08830/030001
C--> 44     (ix) TELECOMMUNICATION INFORMATION:
45          (A) TELEPHONE: 619/678-5070
46          (B) TELEFAX: 619/678-5099
49 (2) INFORMATION FOR SEQ ID NO: 1:
51      (i) SEQUENCE CHARACTERISTICS:
52          (A) LENGTH: 1225 base pairs
53          (B) TYPE: nucleic acid
54          (C) STRANDEDNESS: single
55          (D) TOPOLOGY: linear
57     (ii) MOLECULE TYPE: cDNA
61     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
63                           AAGAAACTCT CCCCGGGTGG AACAAG          26
65 ATG GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC ATC AAT TAT TAT ACA          74
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66  Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
67   1               5                   10                  15
69  TCG GAG CCC TGC CAA AAA ATC AAT GTG AAG CAA ATC GCA GCC CGC CTC      122
70  Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
71          20                  25                  30
72  CTG CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT GGT TTT GTG GGC AAC      170
73  Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
74          35                  40                  45
76  ATG CTG GTC ATC CTC ATC CTG ATA AAC TGC AAA AGG CTG AAG AGC ATG      218
77  Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
78      50                  55                  60
80  ACT GAC ATC TAC CTG CTC AAC CTG GCC ATC TCT GAC CTG TTT TTC CTT      266
81  Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
82   65                  70                  75                  80
84  CTT ACT GTC CCC TTC TGG GCT CAC TAC TTG GCC GCC CAG TGG GAC TTT      314
85  Leu Thr Val Pro Phe Trp Ala His Tyr Leu Ala Ala Gln Trp Asp Phe
86                  85                  90                  95
88  GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC TAT TTT ATA GGC TTC      362
89  Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
90              100                 105                 110
92  TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG      410
93  Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
94          115                 120                 125
96  GCT GTC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT      458
97  Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
98      130                 135                 140
100 GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GCT GTG TTT GCG TCT      506
101 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
102 145                 150                 155                 160
104 CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC      554
105 Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
106                 165                 170                 175
108 ACC TGC AGC TCT CAT TTT CCA TAC AGT CAG TAT CAA TTC TGG AAG AAT      602
109 Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn
110             180                 185                 190
112 TTC CAG ACA TTA AAG ATA GTC ATC TTG GGG CTG GTC CTG CCG CTG CTT      650
113 Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu
114             195                 200                 205
116 GTC ATG GTC ATC TGC TAC TCG GGA ATC CTA AAA ACT CTG CTT CGG TGT      698
117 Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys
118     210                 215                 220
120 CGA AAT GAG AAG AAG AGG CAC AGG GCT GTG AGG CTT ATC TTC ACC ATC      746
121 Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
122 225                 230                 235                 240
124 ATG ATT GTT TAT TTT CTC TTC TGG GCT CCC TAC AAC ATT GTC CTT CTC      794
125 Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu
126             245                 250                 255
128 CTG AAC ACC TTC CAG GAA TTC TTT GGC CTG AAT AAT TGC AGT AGC TCT      842
129 Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser
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```
130              260              265                 270
132 AAC AGG TTG GAC CAA GCT ATG CAG GTG ACA GAG ACT CTT GGG ATG ACG         890
133 Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr
134         275              280                 285
136 CAC TGC TGC ATC AAC CCC ATC ATC TAT GCC TTT GTC GGG GAG AAG TTC         938
137 His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe
138         290              295              300
140 AGA AAC TAC CTC TTA GTC TTC TTC CAA AAG CAC ATT GCC AAA CGC TTC         986
141 Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe
142 305                  310              315                 320
144 TGC AAA TGC TGT TCT ATT TTC CAG CAA GAG GCT CCC GAG CGA GCA AGC        1034
145 Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser
146             325              330                 335
147 TCA GTT TAC ACC CGA TCC ACT GGG GAG CAG GAA ATA TCT GTG GGC TTG        1082
148 Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu
149             340              345              350
151 TGACACGGAC TCAAGTGGGC TGGTGACCCA GTCAGAGTTG TGCACATGGC TTAGTTTTCA       1142
153 TACACAGCCT GGGCTGGGGG TGGGGTGGGA GAGGTCTTTT TTAAAAGGAA GTTACTGTTA       1202
155 TAGAGGGTCT AAGATTCATC CAT                                 1225
158 (2) INFORMATION FOR SEQ ID NO: 2:
160      (i) SEQUENCE CHARACTERISTICS:
161          (A) LENGTH: 352 amino acids
162          (B) TYPE: amino acid
163          (D) TOPOLOGY: linear
165      (ii) MOLECULE TYPE: peptide
169      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
171 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
172 1               5                   10                  15
175 Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala.Ala Arg Leu
176             20                  25                  30
178 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
179         35               40                  45
182 Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
183     50                  55                  60
186 Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
187 65                  70                  75                  80
189 Leu Thr Val Pro Phe Trp Ala His Tyr Leu Ala Ala Gln Trp Asp Phe
190             85                  90                  95
193 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
194         100              105                 110
197 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
198         115              120                 125
201 Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
202     130              135                 140
205 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
206 145              150                 155                 160
209 Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
210             165                 170                 175
213 Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn
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214          180                   185                   190
217 Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu
218          195                   200                   205
221 Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys
222     210                   215                   220
225 Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
226 225                   230                   235                   240
229 Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu
230               245                   250                   255
233 Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser
234               260                   265                   270
237 Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr
238          275                   280                   285
241 His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe
242     290                   295                   300
245 Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe
246 305                   310                   315                   320
249 Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser
250               325                   330                   335
252 Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu
253               340                   345                   350     352
257 (2) INFORMATION FOR SEQ ID NO: 3:
259      (i) SEQUENCE CHARACTERISTICS:
260          (A) LENGTH: 1225 base pairs
261          (B) TYPE: nucleic acid
262          (C) STRANDEDNESS: single
263          (D) TOPOLOGY: linear
265      (ii) MOLECULE TYPE: cDNA
268      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
270                              AAGAAACTCT CCCCGGGTGG AACAAG          26
272 ATG GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC ATC AAT TAT TAT ACA       74
273 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
274 1               5                   10                  15
276 TCG GAG CCC TGC CAA AAA ATC AAT GTG AAG CAA ATC GCA GCC CGC CTC      122
277 Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
278          20                  25                  30
279 CTG CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT GGT TTT GTG GGC AAC      170
280 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
281          35                  40                  45
283 ATG CTG GTC ATC CTC ATC CTG ATA AAC TGC AAA AGG CTG AAG AGC ATG      218
284 Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
285     50                  55                  60
287 ACT GAC ATC TAC CTG CTC AAC CTG GCC ATC TCT GAC CTG TTT TTC CTT      266
288 Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
289 65                  70                  75                  80
291 CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC GCC CAG TGG GAC TTT      314
292 Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
293               85                  90                  95
295 GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC TAT TTT ATA GGC TTC      362
```

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296 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
297         100                 105                 110
299 TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG     410
300 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
301         115                 120                 125
303 GCT GTC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT     458
304 Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
305         130                 135                 140
307 GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GCT GTG TTT GCG TCT     506
308 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
309 145                 150                 155                 160
311 CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC     554
312 Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
313                 165                 170                 175
315 ACC TGC AGC TCT CAT TTT CCA TAC AGT CAG TAT CAA TTC TGG AAG AAT     602
316 Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn
317                 180                 185                 190
319 TTC CAG ACA TTA AAG ATA GTC ATC TTG GGG CTG GTC CTG CCG CTG CTT     650
320 Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu
321         195                 200                 205
323 GTC ATG GTC ATC TGC TAC TCG GGA ATC CTA AAA ACT CTG CTT CGG TGT     698
324 Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys
325         210                 215                 220
327 CGA AAT GAG AAG AAG AGG CAC AGG GCT GTG AGG CTT ATC TTC ACC ATC     746
328 Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
329 225                 230                 235                 240
331 ATG ATT GTT TAT TTT CTC TTC TGG GCT CCC TAC AAC ATT GTC CTT CTC     794
332 Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu
333                 245                 250                 255
335 CTG AAC ACC TTC CAG GAA TTC TTT GGC CTG AAT AAT TGC AGT AGC TCT     842
336 Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser
337         260                 265                 270
339 AAC AGG TTG GAC CAA GCT ATG CAG GTG ACA GAG ACT CTT GGG ATG ACG     890
340 Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr
341         275                 280                 285
343 CAC TGC TGC ATC AAC CCC ATC ATC TAT GCC TTT GTC GGG GAG AAG TTC     938
344 His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe
345         290                 295                 300
347 AGA AAC TAC CTC TTA GTC TTC TTC CAA AAG CAC ATT GCC AAA CGC TTC     986
348 Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe
349 305                 310                 315                 320
351 TGC AAA TGC TGT TCT ATT TTC CAG CAA GAG GCT CCC GAG CGA GCA AGC     1034
352 Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser
353                 325                 330                 335
354 TCA GTT TAC ACC CGA TCC ACT GGG GAG CAG GAA ATA TCT GTG GGC TTG     1082
355 Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu
356         340                 345                 350
358 TGACACGGAC TCAAGTGGGC TGGTGACCCA GTCAGAGTTG TGCACATGGC TTAGTTTTCA     1142
360 TACACAGCCT GGGCTGGGGG TGGGGTGGGA GAGGTCTTTT TTAAAAGGAA GTTACTGTTA     1202
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 08/27/2004
PATENT APPLICATION: **US/10/700,313**   TIME: 14:23:01

Input Set : **N:\Crf3\RULE60\10700313.raw**
Output Set: **N:\CRF4\08272004\J700313.raw**

<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos.1

VERIFICATION SUMMARY   DATE: 08/27/2004
PATENT APPLICATION: **US/10/700,313**   TIME: 14:23:01

Input Set : **N:\Crf3\RULE60\10700313.raw**
Output Set: **N:\CRF4\08272004\J700313.raw**

L:26 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:27 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:34 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:37 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)
L:39 M:220 C: Keyword misspelled or invalid format, [(viii) ATTORNEY/AGENT INFORMATION:]
L:44 M:220 C: Keyword misspelled or invalid format, [(ix) TELECOMMUNICATION INFORMATION:]
L:474 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]
L:479 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0